Our Ref. No. 55.US4.DIV

The Commissioner is hereby authorized to credit any overpayment or charge any additional fees in connection with the filing of this Preliminary Amendment to our Deposit Account No. 50-1181.

Respectfully submitted,
GENSET CORPORATION

Date: 14 May 01, 2001

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 1-30 have been canceled.

31. (Amended) A method of determining whether a candidate genomic region harbors a gene associated with a detectable trait comprising determining whether the association of a plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of a plurality of biallelic markers located in a plurality of random genomic regions [wherein the determination of whether the association of said plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of said plurality of biallelic markers located in a plurality of random genomic regions comprises:

constructing a candidate region distribution of test values using said biallelic markers in said candidate genomic region, said candidate region distribution of test values being indicative of the difference in the haplotype frequencies of said biallelic markers in said candidate region in individuals who possess said detectable trait and control individuals who do not possess said detectable trait;

constructing a random region distribution of test values using said biallelic markers in said genomic region said random region distribution of test values being indicative of the difference in the haplotype frequencies of said biallelic markers in said random genomic regions in individuals who possess said detectable trait and control individuals who do not possess said detectable trait; and

comparing said candidate region distribution of test values with said random region distribution of test values.]

Claims 32-47 have been canceled.

Claims as Pending after Preliminary Amendment

31. A method of determining whether a candidate genomic region harbors a gene associated with a detectable trait comprising determining whether the association of a plurality of biallelic markers located in said candidate genomic region with said detectable trait is significantly different than the association of a plurality of biallelic markers located in a plurality of random genomic regions.